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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

October 15, 1999, 00:29:31; Search time 29:22 Seconds (without alignments) 255.037 Million cell updates/sec

US-09-185-258-6 1001 1 EKPLHALLHGRGVCLNEKSY.....GMEYVDGDFQCHTFDSSNVE 186 Title: Perfect score: Sequence:

BLOSUM62 Scoring table: 122810 seqs, 40065486 residues

Searched:

Database :

PIR_60:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		insulin-like growt	in-like	nsulin-like	in-1	in-like	in-like	nsulin-like	in-like	in-like	in-like	in-like	like	nsulin-like	like	like	nsulin-like	like	nsulin-like	like	$\overline{}$	ike	ike	like	like	lik	like	like	like	αı	like	-like	like	testican - human	thyroglobulin prec	a C C	M5 protein precurs	•	pan-epithelial gly	
SUMMARIES	ID		A53748	JC4584	\circ	JC1463	10	A35037	IOHU3	A36748	I48502	B45403	A39842	I48605	JN0464	A45403	147031	601662	B37252	I48599	I48603	JC1464	A60967	I48600	I46916	A36082	A33274	A41927	IOHUI	T01404	823009	I48601	250	C45403	m	UIHO	S	2861	617	A46489	G00043
	DB	- 1									8																														
	Length		272	271	271	271	291	266	291	292	291	111	240	238	226	258	237	258	258	254	254	254	310	272	317	272	304	328	255	122	263	305	305	122	436	2767	1247	492	212	314	1376
dР	Query		99.4	97.9	96.7	96.4	35.3	34.6	34.4	32.7	32.1	30.8	26.7	25.2	24.2	24.2	23.8	23.7	23.7	22.5	22.5	22.5	20.1	19.5	19.2	18.4	17.9	17.9	17.7	17.3	17.3	17.2	17.1	16.4	12.2	11.0	10.7	10.2	φ. œ.	φ. ω	9.1
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Gaps

δÖ a γ_{χ}

Query Match
99.4%; Score 995; DB 2; Length 272;
Best Local Similarity 99.5%; Pred. No. 1.1e-76;
Matches 185; Conservative 0: Mismatches 1; Indels

61 LKAEAV KUDRPYKLFQSKFVGGAENTAHPRIISEPEMRQESEQGPCRRHMEASLQELKAS 120

thyroglobulin prec thyroglobulin 2 pr nidogen precursor M6 protein - Strep M2 protein precurs IgA receptor - Str	precursor - human -1995 #Lext_change 20-Mar-1998 Suwanichkul, A.; Weber, G.; Mor gene and promoter for human insu L27558; GB:L27559; NID:9452057: Ling, N. ulin-like growth factor binding J:	There is considered to the new number insurantive growth factor binding process. Accession: JH0391, MGID:91207396 Accession: JH0391 Accession: JH0391 Residues: 1-272 (KIE) Cross-references: GB:M65062; NID:9184819; PID:9184820 Experimental source: Osteosarcoma Andress, D.L.: Birnbaum, R.S. Cochem: Blophys. Res. Commun. 176, 213-218, 1991 Title: A novel human insulin-like growth factor binding protein secreted by osteoblacession: PH0143: MUID:91207395 Accession: PH0143 Accession: PH0144 Access
UIBO A36124 MMMSND A26297 S23325 S37046	.revision 31-Dec JH0391; PH0143 PH01391; PH0143 PH01399 B.; PH0143 PH0143 PH0143 PH0193798 PH01D: 94193798 PHP; PH01D: 94193798 PHP; PH01D: 91244847 PH01D: 91244847 PH ta Uer, D.M.; Zapf, La Uer, D.M.; Zapf	new numen in: 91207396 ID:9184819; 76, 213-218, ike growth fi.: 91207395 V-2 actors occur actors occur actors prediction to with factor rowth factor rowth factor
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96.5 91.5 91.5 91.5	AS3748 insulin like growth factor-binding protein 5 N.Alternate names: IGFBP-5 C.Species: Homo Sapiens (man) C.Species: As3748; B40403; JH0391; PH0143 R.Altander, S.V.; Larsson, C.: Ehimoborg, E.; A.Title: Characterization of the chromosomal A.Reference number: A53748; MuID:94193798 A.Rocession: BA3748 A.Reference: USB:LZ7556; GB:LZ7557; GB: R.Shimasaki, S.; Shimonaka, M.; Zhang, H.P.; J. Biol. Chem. 266, 10646-10553, 1991 A.Title: Identification of five different ins A.Reference number: A40403: MuID:91244847 A.Recession: B40403 A.Status: preliminary A.Residues: 1-272 < GBI A.Residues: 1-272 < GBI A.Riefer, M.C.; Loh, K.S.; Bauer, D.M.; Zapf, B.Hochem: Biophys. Res. Commun. 176, 219-225,	A, Flexer accounts containing of a new numan insuling A, Reference number: JH0391, MGID:91207396 A, Accession: JH0391 A, Molecule: 1-272 < KIES A, Residues: 1-272 < KIES A, Experimental source: Osteosarcoma A, Randreas, D.L.: Birnbaum, R.S. Biochem: Biophys. Res. Commun. 176, 213-218, 1991 A, Andreas, D.L.: Birnbaum, R.S. Biochem: Biophys. Res. Commun. 176, 213-218, 1991 A, Aritle: A novel human insulin-like growth factor A, Reference number: PH0143: MUID:91207395 A, Accession: PH0143 A, Molecule type: protein A, Residues: 24-37'X',39-41,'X',43 < AND> A, Experimental source: cell line V-2 C, Comment: Insulin-like growth factors occur in set C, Genetics: GBB:126837 A, Gene GBB:126897 A, Gene GBB:126897 C, Superfamily: thyroglobulin type I repeat homolog F; 1-23/Domain: signal sequence #status predicted F; 192-263/Domain: thyroglobulin type I repeat homolog
O H W M M M	RESULT 1 A53140 Insulable like NyAlternate r Cyspecies: HC	A. A. Fefere A. A. Coross A. Moross A. A. Cross A. A. Triters A. A. Cross A. A. Cross A. Cros
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Affile: Organization, expression, and chromosomal location of the mouse insulin-like A;Reference number: A54259; MUID:94307727
A;Recession: A54259
A;Molecule type: DNA
A;Residues: 1-111 < KOU>
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C;Date: 30-Sep-1993 *Sequence_revision 30-Sep-1993 *text_change 10-Sep-1997
C;Date: 30-Sep-1993 *Sequence_revision 30-Sep-1993 *text_change 10-Sep-1997
C;Accession: JC1463; A40403: F40403
R;Zhu, X.; Ling, N.; Shimasaki, S.
Blochen Biophys. Res. Commun. 190, 1045-1052, 1993
A;Fille: Cloning of the rat insulin- like growth factor binding protein-5 gene and DN A:Reference number: JC1463: MUID:93176146
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R;Shimsaaki, S.; Shimonaka, M.; Zhang, H.P.; Ling, N.
B:Shimsaaki, S.; Shimonaka, M.; Zhang, H.P.; Ling, N.
Biol. Chem. 266, 10646-10653, 1991
A:Itile: Identification of five different insulin-like growth factor binding proteins A;Reference number: A40403; MUID:91244847
                                                                                                                                                         A.Cross-references: EMBL:X81583; NID:9550384; PID:9550385
R.James, P.L.; Jones, S.B.; Busby Jr., W.H.: Clemmons, D.R.; Rotwein, P.
J. Biol. Chem. 268, 22305-2312, 1993
A.Title: A highly conserved insulin-like growth factor-binding protein (IGFBP-5) is A.Reference number: A48699; MUID:94042976
A.Status: preliminary
A.Status: preliminary
A.Status: RNA
A.Residues: 1-271 <JAM>
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A;Residues: 1-271 <SHI>
A;Cross-references: GB:M62781: NID:g204745; PID:g204746
A;Accession: F40403
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Pred. No. 2e-74;
2; Mismatches 6
                                       A;Accession: 148604
A;Status: preliminary; translated from GB/EMBL/DDBJ
   Reference number: I48600; MUID:95121750
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Best Local Similarity 95.7
Matches 178; Conservative
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C;Genetics:
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A; Molecule type: DNA
A; Residues: 1-271 <ZHU>
                                                                                                 A; Molecule type: mRNA
A; Residues: 1-271 <RES>
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C;Species: Sus scrofa domestica (domestic pig)
C;Dacte: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 13-Nov-1998
C;Accession: UC4564; G23734
R;White, M.E.; Diao, R.; Hathaway, M.R.; Mickelson, J.; Dayton, W.R.
Biochem. Biophys. Res. Commun. 218, 248-253, 1996
A;Title: Molecular cloning and sequence analysis of the porcine insulin-like growth fact
A;Reference number: UC4584; MUID:96136309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 20-25, X', 27-28, X', 30-36, X', 38-39 < SHI>
C; Comment: This protein has essential roles in the regulation and coordination of insuli lays a role during myoblast proliferation and differentiation, and is important in the 9 C; Superfamily: thyroglobulin type I repeat homology
C; Keywords: differentiation; growth factor; skeletal muscle
E; 1-19/Domain: signal sequence #status predicted < SIG>
E; 20-271/Product: ansulin-like growth factor binding protein-5 #status experimental < MAI F; 191-262/Domain: thyroglobulin type I repeat homology < THYI>
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C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 17-Mar-1999
C; Accession: 148604; A48699; A548699; A548699; A548699; A548699; A548699; Ascession of the Schuller, A.G.; Groffen, C.; van Neck, J.W.; Zwarthoff, E.C.; Drop, S.L.
Mol. Cell. Endocrinol. 104, 57-66, 1994
A; Title: cDNA cloning and mRNA expression of the six mouse insulin-like growth factor bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rishimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.
Mol. Endocrinol. 5, 938-948, 1991
A.Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-A.Reference number: A23734; WUID:92049376
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207 PRMVPRAVYLPNCDRKGFYRRQCKPSRGRKRGICWCVDKYGMKLPGMEYVDGDEQCHTF
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A;Experimental source: skeletal muscle
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Best Local Similarity 97.3%; Pred. No. 1.9e-75;
Matches 181; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-271 <WHI>
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266 DSSNVE
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Wed Dec

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inhibit

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A.Molecule type: DNA
A.Residues: 1-291 <CUB>
A.Residues: 1-291 <CUB>
A.Cross-references: GB:M3578; GB:J05537; NID:q184522; PID:q386791
A.Cross-references: GB:M3578; GB:J0537; NID:q184522; PID:g386791
R.Mood, W.I.; Cachianes, G.; Henzel, W.J.: Winslow, G.A.; Spencer, S.A.: Hellmiss, R. Mol. Endocrinol. 2, 1176-1185, 1988
A.Title: Cloning and expression of the growth hormone-dependent insulin-like growth fa.Reference number: A.4940; MUID:89112197
A.Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thyroglobulin type I rep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insulin-like growth factor-binding protein 3 homolog - pig
C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Accession: A35037
R; Shimmasaki, S.; Shimonaka, M.; Ui, M.; Inouye, S.; Shibata, F.; Ling, N.
T; Shimasaki, S.; Shimonaka, M.; Ui, M.; Inouye, S.; Shibata, F.; Ling, N.
A; Reference number: A55037; MulD:90130475
A; Reference number: A55037; MulD:90130475
A; Moleçule type: mRNA
A; Moleçule type: mRNA
                                                                                                                   110 MEASLQELKASPRMVPRAVYLPNCDRKGFYKRKQCKPSRGRKRGICWCVDKYGMKLPGME 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 HTRISEL--KAEAVKKDRRKKLTQSKFVGGAENTAHPRIISEPEMRQESEQGPCRRHMEA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SESKRETEYGPCRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KPLHALLHGRGVCLNEKS----YREQVKIERDSREHEEPITSEMAEETYSPKIFRPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 SLQELKASPRMYPRAVYLPNCDRKGFYKRKQCKPSRGRKRGICWCVDKYGMKLPGMEYV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 266,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB:J05228
C; Superfamily: insulin-like growth factor binding protein 1: F:188-260/Domain: thyroglobulin type I repeat homology <THY1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 346; DB 2;
: Pred. No. 3.3e-22:
32; Mismatches 75
                    | | | || : : | | : | : :| 104 KFHPIHTKMDVIKKGHAKDSQRYKVDYESQSTDTQNFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.68;
37.78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 37.79
Matches 72; Conservative
                                                                                                                                                                                                                                                    170 YV-DGDFQCHIFDS 182
                                                                                                                                                                                                                                                                                                                 277 VKGKGDVHCYSMES 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 KGDVHCYSMES 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 DGDFQCHTFDS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-266 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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JN0064
Insulin-like growth factor-binding protein 3 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Nov-1993 #sequence_revision 05-Apr-1995 #text_change 05-Sep-1997
C;Accession: JN0064, A33403
R;Spratt, S.K.; Tatsuno, G.P.: Sommer, A.
B;Spratt, S.K.; Tatsuno, G.P.: Som, A.
B;Spratt, S.K.; Tatsuno, G.P.: Som, A.
B;Spratt, S.C.; Spratt, A.
B;Spratt, Source: Liver
B;Conover, C.A.; Ronk, M.; Lombana, F.; Powell, D.R.
B;Accession: A37403
A;Reference number: A37403; MUID:91065246
A;Residues: 28-52 CCON>
B;Genetics:
B;Conover, C.B.: Sourk, M.;Conover, C.B.: Sourk, G.Genetics:
B;Conortoniogy 120; A7103
B;Co
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C.Superfamily: insulin-like growth factor binding protein 1; thyroglobulin type I repeat
C.Keywords: glycoprotein
C.Keywords: glycoprotein
F.1-27/Domain: signal sequence #status predicted <SIG>
F.28-291/Product: insulin-like growth factor-binding protein 3 #status predicted <MAT>
F.28-5/Domain: thyroglobulin type I repeat homology <THYI>
F.118,136,199/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                        <MAT>
A:Status: preliminary
A:Molecule type: protein
A:Residues: 20-25,'X',27-28,'X',30-36,'X',38-43,'X',45-51,'X',53,'XX' <SH2>
C:Genetics: 112/3: 188/3: 228/3
C:Genetics: 112/3: 188/3: 228/3
C:Superfamily: thyroglobulin type I repeat homology
C:Superfamily: thyroglobulin type I repeat homology
F:1-19/Domain: signal sequence *status predicted <SIG>F:20-271/Product: insulin-like growth factor binding protein 5 *status predicted F:191-262/Domain: thyroglobulin type I repeat homology <THYI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 LKAEAVKKDRRKKLTQSKFVGGAENTAHPRVIPAPEMRQESDQGPCRRHMEASLQEFKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EKPLHALLHGRGVCLNEKSYREQVKIERD$REHBEPTTSEMAEETYSPKIFRPKHTRISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKAEAVKKDRRKKLTQSKFVGGAENTAHPRIISEPEMRQESEQGPCRRHMEASLQELKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PRMVPRAVYLPNCDRKGFYKRKQCKPSRGRKRGICWCVDKYGMKLPGMEYVDGDFQCHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KPLHALLHGRGVCLNEKSYRE----QVKIERDSREHEEPTTSEMAEETYSPKI-----
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                                                                                                                                                                                                                                                                                                                                                                                  Length 271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                               96.4%; Score 965: DB 2;
95.2%: Pred. No. 3.5e-74;
live 3; Mismatches 6;
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37.6%: Pred. No. 9.3e-23;
Live 28; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 177; Conserv
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nes 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 DSSNVE 186
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Matches
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A;Molecule type: mRNA
A;Residues: 1-7,9-792 <ALB>
A;Residues: 1-7,9-792 <ALB>
A;Residues: 1-7,9-792 
Biochem: Biophys: Res. Commun. 165, 189-195, 1989
A;Title: Identification of a novel binding protein for insulin-like growth factors in A;Reference number: A33570; MUD:90073708
A:Accession: A33570
                                                                          NiAlternate names: IGF-binding protein
C;Species: Rattus norvegious (Norway rat)
C:Date: 31-May-1991-%sequence_revision 31-May-1991 #text_change 13-Sep-1998
C:Date: 31-May-1991-%sequence_revision 31-May-1991 #text_change 13-Sep-1998
C;Accession: A36748; A34551; A33570; A30820; B30820; A26832: D40403
R;Shimasaki, S.; Koba, A.; Mercado, M.; Shimonaka, M.; Ling, N.
Biochem: Blophys. Res. Commun. 165, 907-912, 1989
A;Title: Complementary DNA structure of the high molecular weight rat insulin-like gr A;Rccession: A36748; MUID:90088511
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A;Residues: 28-42 - CBAX>
R;Shimasaki, S.; Shimonaka, M.: Zhang, H.P.: Ling, N.
J. Blol. Chem. 266, 10646-10653, 1991
A;Fitle: Identification of five different insulin-like growth factor binding proteins A;Reference number: A40403: MUID:91244847
A;Accession: D40403
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Biochem. Biophys. Res. Commun. 147, 408-415, 1887
A;Title: Binding proteins for insulin-like growth factors in adult rat serum. Compari
A;Reference number: A26832: MUID:87326380
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A:Molecule type: protein
A:Molecule type: protein
C;Subadides: 28-39, "X, '41-42, "X', '44-47;188-197 <SH3>
C;Superfamily: insulin-like growth factor binding protein 1; thyroglobulin type I rep C;Reywords: glycoprotein; plasma
F;1-27/Domain: signal:sequence #status predicted <SIG>F;214-286/Domain: thyroglobulin type I repeat homology <THYL>
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                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-292 <SHI>
A:Cross-references: GB:M31837; NID:g204741: PID:g204742
R;Albiston, A.L.; Herington, A.C.
Biochem. Biophys. Res. Commun. 166, 892-897, 1990
A;Title: Cloning and characterization of the growth hormone-dependent insulin-like (A;Reference number: A34651; MUID:90147804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Wolecule type: protein
A:Residues: 28.39, X',41-42, X',44-49 <SH2>
R:Zapf, J.; Born, W.; Chang, J.Y.; James, P.; Froesch, E.R.; Fischer,
Biochem. Biophys. Res. Commun. 156, 1187-1194, 1988
A;Title: Isolation and NH-2-terminal amino acid sequences of rat serum
A;Reference number: A90149; MUID:89050156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
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                                              insulin-like growth factor-binding protein 3 precursor
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37.8%: Pred. No. 1.4e-20;
iive 26: Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Moleculé type: protein
A;Residues: 28-55,'X',57-59,'X',61-68 <2A2>
A;Note: this sequence was derived from a protein of
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A:Moste: this sequence was derived from a protein of
A:Accession: B30820
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Best Local Similarity 37.8 Matches 68; Conservative
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A; Reference number: A35803; MUID:90368661
A; Recession: B35803
A; Molecule type: protein
A; Residues: 28-59, x, 61-63, x, 65 < ZAP>
R; Roghani, M.; Segovia, B.; Whitechurch, O.; Binoux, M.
A; Title: Purification from human cerebrospinal fluid of insulin-like growth factor bindi
A; Reference number: A34651; MUID:93091816
A; Recession: B54651
A; Molecule type: protein
A; Recidues: 28-39, x', 41-42, x', 44-45 < ROG>
A; Rocession: B54651
A; Molecule type: protein
A; Residues: 28-39, x', 41-42, x', 44-45 < ROG>
A; Rocession: B54651
A; Molecule cype: protein
A; Residues: Carebrospinal fluid
A; Note: sequence extracted from NCBI backbone (NCBIP:121073)
B; Thweatt, R; Pieischmann, R: Goldstein, S; DNA Seq. 4, 43-46, 1993
B) NA Seq. 4, 43-46, 1993
A; Title: Analysis of the primary structure of insulin-like growth factor binding protein
A; Reference number: 137622; MUID:94146408
A; Residues: 1-291 <WOO>
A; Cross-references: GB:M35878: NID:g184522; PID:g386791
A; Cross-references: GB:M35878: NID:g184522; PID:g386791
A; Cross-references: GB:M35878: NID:g184522; PID:g386791
B; Spratt, S.K.; Tatsuno, G.P.; Yamanaka, M.K.; Ark, B.C.; Detmer, J.; Mascarenhas, D.; F Growth Factors 3, 63-72, 1990
A; Title: Cloning and expression of human insulin-like growth factor binding protein 3.
A; Reference number: A61038; MUID:g0344267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 7p13-7p12
A:Introns: 135/1: 210/3; 250/3
A:Introns: 135/1: 210/3; 250/3
C:Superfamily: insulin-like growth factor binding protein 1: thyroglobulin type I repeat C:Keywords: glycoprotein
F:1-27/Domain: signal sequence *status predicted <SIG>
F:28-291/Product: insulin-like growth factor-binding protein 3 *status experimental <MAT
                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-11,'A',33-291 <SPR>
R;Zapf, J.; Kiefer, M.; Merryweather, J.; Masiarz, F.: Bauer, D.; Born, W.; Fischer, J.A
J. Biol. Chem. 265, 14892-14898, 1990
A;Title: Isolation from adult human serum of four insulin-like growth factor (IGF) bindi
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F;28-291/Product: insulin-like growth factor-binding protein 3 *status experimental <MAT
F;28-295/Domain: thyroglobulin type I repeat homology <THYI>
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;136,199/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: mrsA
A;Residues: 1-291 <RESA
A;Cross-references: EMBL:X64875: NID:g398163; PID:g398164
G,Genetics:
A;Gene: GDB:IGFBP3
A;Cross-references: GDB:126724; OMIM:146732
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                                                                                                                                                                                                                                                                     A; Accession: A61038
A; Status: not compared with conceptual translation
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Best Local Similarity
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R;Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N. Mol. Endocrinol. 5, 938-948, 1991
Mol. Endocrinol. 5, 938-948, 1991
A;Title: Isolation and molecular cloning of insulin-like growth factor-binding protei
A;Reference number: A23734; MUID:92049376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Martin, J.L.; Willetts, K.E.; Baxter, R.C. J. Biol. Chem. 265, 4124-4130, 1990
A.Title: Purification and properties of a novel insulin-like growth factor-II binding A.Reference number: A35470; WUID:90154107
A.Recession: A35470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A: Molecule type: profesh
A:Residues: 28, A':30-39 cMAR>
R:Zapf, J., Kiefer, M.; Merryweather, J.; Masiarz, F.: Bauer, D.: Born, W.: Fischer,
J. Blod. Chem. 265, 14892-14898, 1990
A:Title: Isolation from adult human serum of four insulin-like growth factor (IGF) bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Andress, D.L.; Birnbaum, R.S.
Biochem. Biophys. Res. Commun. 176, 213-218, 1991
A; Title: A novel human insulin-like growth factor binding protein secreted by osteobl
A; Reference number: PH0143; MUID:91207395
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insulin-like growth factor-binding protein 6 precursor - human N.Alternate names: IGFBP-6; insulin-like growth factor II-binding protein C. Species: Homo Sapiens (man) C. Date: 20 Mar-1992 #sequence_revision 31-Dec-1995 #text_change 10-Sep-1997 C.Accession: A39842; B23734; PH0144; A35470; C35803 K. Kiefer, M.C.; Masiarz, F.R.; Bauer, D.M.: Zapf, J. J. Biol. Chem. 266, 9043-9049; 1991 A:Title: Identification and molecular cloning of two new 30-kDa insulin-like growth A:Reference number: A39842; MUID:91225006
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F:1-27/Domain: signal sequence *status predicted <SIG>
F:12-27/Domain: signal sequence *growth factor-binding protein 6 *status F:28-240/Product: insulin-like growth factor-binding protein 6 *status F:163-234/Domain: thyroglobulin type I repeat homology <PHMI>
F:229/Binding site: carbohydrate (Asn) (covalent) *status predicted
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A;Cross-references: GB:M62402: NID:g184813; PID:g184814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Molecule type: mRNA
A:Residues: 'C',3-240 <SHI>
A:Cross-references: GB:M69054; NID:g183893; PID:g183894
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Pred. No. 1.1e-15:
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A;Map position: 12pter-12qter
C;Superfamily: thyroglobulin type I repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Molecule type: protein
A;Residues: 'XX', 30-31,'P',33-39,'X',41-42 <AND>
A;Experimental source: cell line V-2
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A:Accession: C35803
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A; Residues: 'AA', 30-31,'H', 33-54,'QXG'
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32.4%;
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Best Local Similarity
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F;213-285/Domain: thyroglobulin type I repeat homology <THX1>
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                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 10-Oct-1997
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 10-Oct-1997
C;Accession: 148602
R;Schuller, A.G.; Groffen, C.; van Neck, J.W.; Zwarthoff, E.C.; Drop, S.L.
Mol. Cell. Endocrinol. 104, 57-66, 1994
A;Title: CDNA cloning and mRNA expression of the six mouse insulin-like growth factor ]
A;Reference number: 148600: MUID:95121750
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C.Accession: B45403

C.Accession: B45403

R.Moser, D.R.: Lowe Jr., W.L.: Dake, B.L.: Booth, B.A.: Boes, M.; Clemmons, D.R.: Bar, M.I. Endocrinol. 6. 1805-1814, 1992

A.Title: Endochelial cells express insulin-like growth factor-binding proteins 2 to 6. A.Reference number: A45403: MUID: 93125553

A.Accession: B45403

A.Status: preliminary; not compared with conceptual translation

A.Molecule type: nucleic acid
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999
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                                       51 -FRPKHTRISELKAEAVKKDRRKKLTQSKFVGGAENTAHPRIISEPEMRQESEQGPCRRH.109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 KFHPLHAKMDVIKKGHARDSQRYKVDYESQSTDTQNFS-----SESKRETEYGPCRRE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 MEASLQELKASPRAVPRAVYLPNCDRKGFYRRKQCKPSRGRKRGICWCVDKYGMKLPGME 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 PLRALLNGRGFCANASAAGSLSTYLPSOPAPGNISESEBEHNAGSVESOVVPSTHRVTDS 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. Experimental source: endothelial cells
A. Note: sequence extracted from NCBI backbone (NCBIP:122190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: EMBL:X81581; NID:g550380; PID:g550381
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                                                                                                                                                                                                                                  growth factor binding protein-3 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%; Score 321; DB 2; 36.7%; Pred. No. 4.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.8%; Score 308; DB 2: 98.3%; Pred. No. 1.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: 148602
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-291 <RES>
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Best Local Similarity
Matches 66; Conserv
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Matches 58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: IGFBP-3
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J. Biol. Chem. 266, 10646-10653, 1991
A;Title: Identification of five different insulin-like growth factor binding proteins
A;Reference number: A40403; MUID:91244847
A;Accession: G40403
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A;Title: Endothelial cells express insulin-like growth factor-binding proteins 2 to A;Reference number: A45403; MUID:93125553
A;Recession: A45403
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C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DRDROK------NPRTSAAPIRPSPVODGEMGPCRRHLDSVLQQL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 KASP-RWVPRAVYLPNCDRKGFYKRKQCKPSRGRKRGICWCVDKYGMKLPGMEYVDGDFQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 SELKAEAVKKDRRKKLTQSKFVGGAENTAHPRIISEPEMRQESEQGPCRRHMEASLQELK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 CLOKHLAKIRDRSTSGGKWKVIGAPREEARP------VPQGSCQSELHRALERLA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 ASPRMVPRAVY --- LPNCDRKGFYKRKQCKPSRGRKRGICWCVD-KYGMKLPGMEYVDGD 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LKAEAVKKDRRKKLTOSKFVGGAENTAHPRIIS---EPEMRQESEQGPCRRHMEASLQEL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
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A;Residues: 1-258 <MOS>
A;Cross-references: GB:S52770; NID:g263303; PID:g263304
A;Experimental source: pulmonary artery endothelial cells
A;Note: sequence extracted from NCBI backbone (NCBIN:122183,
C;Superfamily: thyroglobulin type I repeat homology
F:174-249/Domain: thyroglobulin type I repeat homology
                                                                                                                                                                                                                                                         A;Introns: 104/1; 145/3; 186/3
C;Superfamily: thyroglobulin type I repeat homology
F;148-220/Domain: thyroglobulin type I repeat homology <THY1>
                                                                                                                                                                                                                                                                                                                                                                   Score 242.5; DB 2;
Pred. No. 1.3e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Mismatches
                                                                                                                                                      A; Molecule type: protein
A; Residues: 26-29, 'X', 31-32, 'X', 34-38
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Best Local Similarity 31.5%;
Matches 57; Conservative 27
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Matches 62: Conservative
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                                                                                                                                 A;Status: preliminary
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A:Reference number: A23734; MUID:92049376
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C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Mar-1998
C:Accession: JN0464; A23734; G40403
R:Zhu. X.: Ling, N.: Shimasaki, S.
Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. A:Title: Structural characterization of the rat insulin-like growth factor binding prote A:Reference number: JN0464; MUID:93221493
                                                                                                                                                                                                                                                                                                                                                                             Rischuller, A.G.; Groffen, C.; van Neck, J.W.; Zwarthoff, E.C.; Drop, S.L.
Mol. Cell. Endocrinol. 104, 57-66, 1994
A:Title: CDNA cloning and mRNA expression of the six mouse insulin-like growth factor l
A:Reference number: I48600; MUID:95121750
A:Accession: I48605
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                                                                                                                                                                                                                                                                                                          C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 10-Oct-1997
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                            61 LKAEAVKKDRRKKLTQSKFVGGAENTAHPRIIS---EPEMRQESEQGPCRRHMEASLQEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: thyroglobulin type I repeat homology F;160-232/Domain: thyroglobulin type I repeat homology <THYl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .nsulin-like growth factor-binding protein 6 precursor · rat
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A;Residudes: 1-25 csH1>
A:Cross-references: GB:M69055; NID:g206586; PID:g206587
R:Shimasaki, S.; Shimonaka, M.; Zhang, H.P.; Ling, N.
                                                                                                                                                                                                                                                                                insulin-like growth factor binding protein-6 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 252; DB 2;
Pred. No. 2.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: preliminary; translated from GB/EMBL/DDBJ
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A:Residues: 1-226 <ZHU>
A:Cross-references: GB:L11006
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Best Local Similarity
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A;Residues: 1-238 <RES>
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                                                                                                     181 DS 182
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C.Accession: 147031

R.Carr, J.M.; Grant, P.A.; Francis, G.L.; Owens, J.A.; Wallace, J.C.; Walton, P.E.

Nol. Endocrinol. 13, 219-256, 1994

A; Title: Isolation and characterization of ovine IGFBP-4: protein purification and cDNA;

A; Reference number: 147031: MUID:95151165

A; Accession: 147031

A; Accession: 147031

A; Sectius: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-237 CARPA

A; Resi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Ovis sp. (sheep)
C;Date: 15-Oct.1996 #sequence_revision 15-Oct-1996 #text_change 10-Oct-1997
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C;Superfamily: thyroglobulin type I repeat homology
F;153-228/Domain: thyroglobulin type I repeat homology <THY1>
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